**Transcript**

***Dr Ira Cook – Computational tools for proteomics***

So I work on computational tools to help find out what proteins there are in the human body and other organisms. Most people would know about proteins as something that you find in an egg or a steak but many people don’t know that there are hundreds of thousands of proteins all of which have a different function in your body and in the, in other organisms and we would like to find those out.

Part of the process of discovering what proteins are in your body involves a technique called mass spectrometry and that involves breaking the proteins down into successively smaller pieces and we measure the masses of those pieces. Where I come in is building computational tools that will be to take those masses and then figure out what proteins were actually in the samples. So, I guess the outcome I would like to achieve is to build better tools that can do that more accurately, faster and are actually enabling for other researchers.

One of the great things about working with building tools for researchers is that you get to interact with a variety of people who have different projects and one project that I am working on involves looking at the proteins on the surface of the cell and looking at how those are different between cancer cell and non-cancer cells and you can imagine of course that has pretty important medical implications for detecting cancers early and possibly for helping to treat them. Another project involves trying to find new proteins that we think might be involved in allowing apple pathogenic fungus to infect apple and pear crops.